IN THE CLAIMS

Please amend the claims as shown in the following detailed claim listing. The detailed claim listing is intended to reflect amendment of previously pending claims 1 and 12. The specific amendments to individual claims are detailed in the following detailed claim listing.

1. (Currently amended) A method of determining the presence of a mutation in a target polynucleotide, comprising the steps of:

(a) providing at least two identical polynucleotide probe arrays, each array comprising discrete probe features, each probe feature comprising multiple ~~perfect match probes and mismatch~~ probes, all having the same sequence, within a discrete known location within the array, wherein each probe in the array comprises a double stranded region and a single-stranded n-mer overhang region such that the overhangs in each array constitute a complete set of n-mers;

(b) hybridizing the target polynucleotide to said overhangs of probe polynucleotides in one array to generate a target hybridization pattern;

(c) hybridizing a reference polynucleotide to said overhangs of probe polynucleotides in a second array to generate a reference hybridization pattern; and

(d) determining the presence of a mutation in the target polynucleotide by normalizing intensity differences of hybridized perfect match probes in the reference and target hybridization patterns, comparing intensity differences ~~of mismatch~~ probes in the reference and target hybridization patterns and determining whether a mutation is present in the target polynucleotide~~polypeptide;~~

~~wherein normalizing intensity differences comprises dividing each perfect match probe hybridization intensity by a sum of hybridization intensities for all related single base mismatch probes plus a hybridization intensity for the perfect match probe.~~

2. (Original) The method of claim 1, wherein in step b), the hybridized target polynucleotide is ligated to the probe.

3. (Original) The method of claim 1, wherein in step c), the hybridized reference polynucleotide is ligated to the probe.

4. (Original) The method of claim 1, wherein the overhangs have free 5'-ends.

5. (Original) The method of claim 1, wherein the overhangs have free 3'-ends.

6. (Original) The method of claim 1, wherein the n-mer comprises from about 4 to about 50 nucleotides.

7. (Original) The method of claim 1, wherein the mutation is a substitution mutation.

8. (Original) The method of claim 1, wherein the mutation is a deletion mutation.

9. (Previously Presented) The method of claim 1, wherein the mutation is an insertion mutation.

10. (Original) The method of claim 1, in which said target polynucleotide is selected from the group consisting of: a cystic fibrosis transmembrane conductance regulator gene, a p53 gene, a mitochondrial DNA, or an HIV gene.

11. (Previously Presented) The method of claim 1, wherein the arrays are arranged in parallel.

12. (Currently amended) A method of determining whether two or more target polynucleotides are identical, comprising the steps of:

(a) providing at least two identical polynucleotide probe arrays, each array comprising discrete probe features, each probe feature comprising multiple ~~perfect match probes and mismatch~~ probes, all having the same sequence, within a discrete known location within the array, wherein each probe in the array comprises a double stranded region and a single-stranded n-mer overhang region such that the overhangs in each array constitute a complete set of n-mers;

(b) hybridizing first target polynucleotide to said overhangs of probe polynucleotides in one array to generate a first hybridization pattern;

(c) hybridizing second target polynucleotide to said overhangs of probe polynucleotides in a second array to generate a second hybridization pattern; and

(d) normalizing intensity differences of hybridized perfect match probes in the first and second hybridization patterns, comparing intensity differences of mismatch probes in the first and second hybridization patterns and determining whether two or more target polynucleotides are identical;

~~wherein normalizing intensity differences comprises dividing each perfect match probe hybridization intensity by a sum of hybridization intensities for all related single base mismatch probes plus a hybridization intensity for the perfect match probe~~.

13. (Previously Presented) The method of claim 12, wherein in step b), the hybridized first target polynucleotide is ligated to the probe.

14. (Previously Presented) The method of claim 12, wherein in step c), the hybridized second target polynucleotide is ligated to the probe.

15. (Original) The method of claim 12, wherein the overhangs have free 5'-ends.

16. (Original) The method of claim 12, wherein the overhangs have free 3'-ends.

17. (Original) The method of claim 12, wherein the n-mer comprises from about 4 to about 50 nucleotides.

18. (Previously Presented) The method of claim 12, wherein the arrays are arranged in parallel.